



SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc.
Glucksmann, Maria
Meyers, Rachel

<120> 80090, 52874, 52880, 63497, AND 33425
METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF

<130> 38155-20044.00

<140> US 10/080,960

<141> 2001-10-19

<150> US 60/242,040

<151> 2000-10-20

<150> US 60/242,038

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Trp Pro Leu Ser Asn Thr Arg Ser Ser Glu His Ile Lys Glu Val Met
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Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr Thr Ala Thr Phe	
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Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu Leu Met Thr Tyr	
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Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn Lys Asp Leu Pro	
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 50 55 60
 His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe Asn Arg Lys
 65 70 75 80
 Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp Trp Ser Pro
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 Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala Asp Ala Cys
 100 105 110
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 115 120 125
 Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu Pro Leu Pro
 130 135 140
 Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu Ser Pro Lys
 145 150 155 160
 Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr
 165 170 175
 Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr Thr Gln Tyr
 180 185 190
 Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu Val Pro Leu
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 Gln Ser Lys Asn Lys Leu Arg Lys Arg Leu Ala Pro Leu Val Tyr Val
 210 215 220
 Gln Ser Asp Cys Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu
 225 230 235 240
 Leu Met Thr Tyr Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn
 245 250 255
 Lys Asp Leu Pro Gln Gln Leu Lys Asn Pro Ala Ser Met Asp Ala Asp
 260 265 270
 Gly Phe Tyr Arg Ile Ile Ala Gln Tyr Lys Phe Ile Leu Ala Phe Glu
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Val Asn Gln Asp Asn Tyr Ile Asp Ala Phe Glu Cys Met Val Cys Thr
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 Arg Trp Glu Ala Glu Asp Thr His Leu Ser Cys Pro Glu Pro Thr Val
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Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys Leu Val Gly Phe Val	
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Gly Asn Leu Cys Val Ile Gly Ile Leu Leu His Asn Ala Trp Lys Gly	
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Leu Ser Leu Leu Leu Phe Ser Ala Pro Ile Arg Ala Thr Ala Tyr Ser	
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Lys Ser Val Trp Asp Leu Gly Trp Phe Val Cys Lys Ser Ser Asp Trp	
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Phe Ile His Thr Cys Met Ala Ala Lys Ser Leu Thr Ile Val Val Val	
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Ala Lys Val Cys Phe Met Tyr Ala Ser Asp Pro Ala Lys Gln Val Ser	
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Ile His Asn Tyr Thr Ile Trp Ser Val Leu Val Ala Ile Trp Thr Val	
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Ala Ser Leu Leu Pro Leu Pro Glu Trp Phe Phe Ser Thr Ile Arg His	
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Leu Pro Leu Phe Phe Ala Ser Phe Tyr Phe Trp Arg Ala Tyr Asp Gln	
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Tyr	Phe	Gln	Ile	Leu	Leu	Leu	Ala	Ile	His	Arg	Asn	Arg	Asn	His	Ile		
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Leu	Val	Ala	Ile	Trp	Thr	Val	Ala	Ser	Leu	Leu	Pro	Leu	Pro	Glu	Trp
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Asp	Val	Pro	Ala	Val	Ala	Glu	Glu	Phe	Met	Ser	Met	Phe	Gly	Lys	Leu
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 405 410 415
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 tctgactggt ttatccacac atgcatggca gccaaagacc tgacaatcgt tgtggtggcc 360
 aaagtatgct tcatgtatgc aagtgaccca gccaaagacc tgagtatcca caactacacc 420
 atctggtcag tgctggtggc catctggact gtggctagcc tgttaccctt gccggaatgg 480
 ttctttagca ccatcaggca tcatgaaggt gtggaaatgt gcctcgtgga tgtaccagct 540
 ttggctgaag agtttatgtc gatgtttggt aagctctacc cactcctggc atttggcctt 600
 ccattatttt ttgccagctt ttattttctg agagcttatg accaatgtaa aaaacgagga 660
 actaagactc aaaatcttag aaaccagata cgctcaaagc aagtcacagt gatgctgctg 720
 agcattgcca tcatctctgc tctcttgagg ctccccgaat gggtagcttg gctgtgggta 780
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 aaaactgaga aggcagagat tcccatcctt cctgacgtag agcagttttg gcctgagagg 1140
 gacacagtcc cttctgtaca attgaagagc accaacccta cagattgtgg tagctcaggt 1200
 aactcagcgt ggtaccgcaa aactgaaaaa tcagcatggt gccctaagac ggaaatccat 1260
 tcaacattct acttccagat actgcttcta gcaattcaca gaaacagaaa ccacatctca 1320
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 ccttaa 1386

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 <212> DNA
 <213> Homo sapiens

<220>
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gctcagctgc tccatcgctt cactttccca ggctcgcgcc cgaagcagag ccatgagaac	180
cccagggtgc ctggcgagcc gctagcgcc atg ggc ccc ggc gag gcg ctg ctg	233
Met Gly Pro Gly Glu Ala Leu Leu	
1 5	
gcg ggt ctt ctg gtg atg gta ctg gcc gtg gcg ctg cta tcc aac gca	281
Ala Gly Leu Leu Val Met Val Leu Ala Val Ala Leu Leu Ser Asn Ala	
10 15 20	
ctg gtg ctg ctt tgt tgc gcc tac agc gct gag ctc cgt act cga gcc	329
Leu Val Leu Leu Cys Cys Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala	
25 30 35 40	
tca ggc gtc ctc ctg gtg aat ctg tgc ctg ggc cac ctg ctg ctg gcg	377
Ser Gly Val Leu Leu Val Asn Leu Ser Leu Gly His Leu Leu Leu Ala	
45 50 55	
gcg ctg gac atg ccc ttc acg ctg ctc ggt gtg atg cgc ggg cgg aca	425
Ala Leu Asp Met Pro Phe Thr Leu Leu Gly Val Met Arg Gly Arg Thr	
60 65 70	
ccg tgc gcg ccc ggc gca tgc caa gtc att ggc ttc ctg gac acc ttc	473
Pro Ser Ala Pro Gly Ala Cys Gln Val Ile Gly Phe Leu Asp Thr Phe	
75 80 85	
ctg gcg tcc aac gcg gcg ctg agc gtg gcg gcg ctg agc gca gac cag	521
Leu Ala Ser Asn Ala Ala Leu Ser Val Ala Ala Leu Ser Ala Asp Gln	
90 95 100	
tgg ctg gca gtg ggc ttc cca ctg cgc tac gcc gga cgc ctg cga ccg	569
Trp Leu Ala Val Gly Phe Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro	
105 110 115 120	
cgc tat gcc ggc ctg ctg ctg ggc tgt gcc tgg gga cag tgc ctg gcc	617
Arg Tyr Ala Gly Leu Leu Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala	
125 130 135	
ttc tca ggc gct gca ctt ggc tgc tgc tgg ctt ggc tac agc agc gcc	665
Phe Ser Gly Ala Ala Leu Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala	
140 145 150	
ttc gcg tcc tgt tgc ctg cgc ctg ccg ccc gag cct gag cgt ccg cgc	713
Phe Ala Ser Cys Ser Leu Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg	
155 160 165	
ttc gca gcc ttc acc gcc acg ctc cat gcc gtg ggc ttc gtg ctg ccg	761
Phe Ala Ala Phe Thr Ala Thr Leu His Ala Val Gly Phe Val Leu Pro	
170 175 180	
ctg gcg gtg ctc tgc ctc acc tgc ctc cag gtg cac cgg gtg gca cgc	809
Leu Ala Val Leu Cys Leu Thr Ser Leu Gln Val His Arg Val Ala Arg	
185 190 195 200	
agc cac tgc cag cgc atg gac act gtc acc atg aag gcg ctc gcg ctg	857
Ser His Cys Gln Arg Met Asp Thr Val Thr Met Lys Ala Leu Ala Leu	
205 210 215	

ctc gcc gac ctg cac ccc agt gtg cgg cag cgc tgc ctc atc cag cag 905
 Leu Ala Asp Leu His Pro Ser Val Arg Gln Arg Cys Leu Ile Gln Gln
 220 225 230

aag cgg cgc cgc cac cgc gcc acc agg aag att ggc att gct att gcg 953
 Lys Arg Arg Arg His Arg Ala Thr Arg Lys Ile Gly Ile Ala Ile Ala
 235 240 245

acc ttc ctc atc tgc ttt gcc ccg tat gtc atg acc agg ctg gcg gag 1001
 Thr Phe Leu Ile Cys Phe Ala Pro Tyr Val Met Thr Arg Leu Ala Glu
 250 255 260

ctc gtg ccc ttc gtc acc gtg aac gcc cag tgg ggc atc ctc agc aag 1049
 Leu Val Pro Phe Val Thr Val Asn Ala Gln Trp Gly Ile Leu Ser Lys
 265 270 275 280

tgc ctg acc tac agc aag gcg gtg gcc gac ccg ttc acg tac tct ctg 1097
 Cys Leu Thr Tyr Ser Lys Ala Val Ala Asp Pro Phe Thr Tyr Ser Leu
 285 290 295

ctc cgc cgg ccg ttc cgc caa gtc ctg gcc ggc atg gtg cac cgg ctg 1145
 Leu Arg Arg Pro Phe Arg Gln Val Leu Ala Gly Met Val His Arg Leu
 300 305 310

ctg aag aga acc ccg cgc cca gca tcc acc cat gac agc tct ctg gat 1193
 Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asp Ser Ser Leu Asp
 315 320 325

gtg gcc ggc atg gtg cac cag ctg ctg aag aga acc ccg cgc cca gcg 1241
 Val Ala Gly Met Val His Gln Leu Leu Lys Arg Thr Pro Arg Pro Ala
 330 335 340

tcc acc cac aac ggc tct gtg gac aca gag aat gat tcc tgc ctg cag 1289
 Ser Thr His Asn Gly Ser Val Asp Thr Glu Asn Asp Ser Cys Leu Gln
 345 350 355 360

cag aca cac tga gggcctggca gggctcatcg cccccacctt ctaagaagcc 1341
 Gln Thr His *

ctgtggaaag a 1352

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 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 8
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 20 25 30
 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
 35 40 45
 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
 50 55 60

Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
 65 70 75 80
 Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
 85 90 95
 Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
 100 105 110
 Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
 115 120 125
 Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
 130 135 140
 Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
 145 150 155 160
 Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
 165 170 175
 His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
 180 185 190
 Leu Gln Val His Arg Val Ala Arg Ser His Cys Gln Arg Met Asp Thr
 195 200 205
 Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val
 210 215 220
 Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr
 225 230 235 240
 Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro
 245 250 255
 Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn
 260 265 270
 Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val
 275 280 285
 Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val
 290 295 300
 Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala
 305 310 315 320
 Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu
 325 330 335
 Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asn Gly Ser Val Asp
 340 345 350
 Thr Glu Asn Asp Ser Cys Leu Gln Gln Thr His
 355 360

<210> 9

<211> 1092

<212> DNA

<213> Homo sapiens

<400> 9

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ctatccaacg	cactggtgct	gctttgttgc	gcctacagcg	ctgagctccg	tactcgagcc	120
tcaggcgctc	tcctggtgaa	tctgtcgctg	ggccacctgc	tgctggcggc	gctggacatg	180
cccttcacgc	tgctcggtgt	gatgcgcggg	cggacaccgt	cgccgcccgg	cgcatgccaa	240
gtcattggct	tcctggacac	cttcctggcg	tccaacgcgg	cgctgagcgt	ggcggcgctg	300
agcgcagacc	agtggctggc	agtgggcttc	ccactgcgct	acgccggacg	cctgcgaccg	360
cgctatgccg	gcctgctgct	gggctgtgcc	tggggacagt	cgctggcctt	ctcaggcgct	420
gcacttggtg	gctcgtggct	tggctacagc	agcgccttcg	cgctcctgtt	gctgcgcctg	480
ccgcccagag	ctgagcgtcc	gcgcttcgca	gccttcaccg	ccacgctcca	tgccgtgggc	540
ttcgtgctgc	cgctggcggt	gctctgcctc	acctcgctcc	aggtgcaccg	ggtggcacgc	600
agccactgcc	agcgcattga	cactgtcacc	atgaaggcgc	tcgcgctgct	cgccgacctg	660
caccccagtg	tgcggcagcg	ctgcctcatc	cagcagaagc	ggcgcgcgca	ccgcgccacc	720

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aggctggcgg	agctcgtgcc	cttcgtcacc	gtgaacgccc	agtggggcat	cctcagcaag	840
tgcctgacct	acagcaaggc	ggtggccgac	ccgttcacgt	actctctgct	ccgccggccg	900
ttccgccaag	tcctggccgg	catggtgcac	cggtctgctga	agagaacccc	gcgccagca	960
tccacccatg	acagctctct	ggatgtggcc	ggcatggtgc	accagctgct	gaagagaacc	1020
ccgcgccag	cgtccacca	caacggctct	gtggacacag	agaatgattc	ctgcctgcag	1080
cagacacact	ga					1092

<210> 10
 <211> 1178
 <212> DNA
 <213> Homo sapiens

<220>
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acaaacatca	gtgacagaca tcagtggcag a atg gcc tcc cgg tat gtg gca	172
	Met Ala Ser Arg Tyr Val Ala	
	1 5	

gtg gga atg atc tta tca cag acc	gtg gtg gga gtc ctg ggg agc ttc	220
Val Gly Met Ile Leu Ser Gln Thr	Val Val Gly Val Leu Gly Ser Phe	
10	15 20	

tct gtt ctt ctc cat tat ctc tcc ttt tac tgc act ggg tgc agg tta	268
Ser Val Leu Leu His Tyr Leu Ser Phe Tyr Cys Thr Gly Cys Arg Leu	
25 30 35	

agg tcc aca gat ttg att gtt aag cac ctg att gta gcc aac ttc tta	316
Arg Ser Thr Asp Leu Ile Val Lys His Leu Ile Val Ala Asn Phe Leu	
40 45 50 55	

gct ctc cgc tgt aaa gga gtc ccc cag aca atg gca gct ttt ggg gtt	364
Ala Leu Arg Cys Lys Gly Val Pro Gln Thr Met Ala Ala Phe Gly Val	
60 65 70	

aga tat ttt ctc aat gct ctt ggg tgc aaa ctt gtt ttc tat ctc cat	412
Arg Tyr Phe Leu Asn Ala Leu Gly Cys Lys Leu Val Phe Tyr Leu His	
75 80 85	

aga gtg ggc agg gga gtg tcc att ggc acc acc tgc ctc ttg agt gtc	460
Arg Val Gly Arg Gly Val Ser Ile Gly Thr Thr Cys Leu Leu Ser Val	
90 95 100	

ttc cag gtg atc acg gtc agc tcc agg aaa tcc agg tgg gca aaa ctt	508
Phe Gln Val Ile Thr Val Ser Ser Arg Lys Ser Arg Trp Ala Lys Leu	
105 110 115	

aaa gag aaa gcc ccc aag cat gtt ggc ttt tct gtt ctc ctg tgc tgg	556
Lys Glu Lys Ala Pro Lys His Val Gly Phe Ser Val Leu Leu Cys Trp	
120 125 130 135	

atc gtg tgc atg ttg gta aac atc atc ttt ccc atg tat gtg gct ggc	604
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Ile Val Cys Met Leu Val Asn Ile Ile Phe Pro Met Tyr Val Ala Gly	
140 145 150	
aaa tgg aac tac aca aac atc aca gtg aac gag gat ttg gga tac tgt	652
Lys Trp Asn Tyr Thr Asn Ile Thr Val Asn Glu Asp Leu Gly Tyr Cys	
155 160 165	
tct ggg gga ggc aac aac aaa atc gca cag aca ctg cgt gca atg ttg	700
Ser Gly Gly Gly Asn Asn Lys Ile Ala Gln Thr Leu Arg Ala Met Leu	
170 175 180	
tta tca ttc cct gat gtg ttg tgt ctg ggg ctc atg ttc tgg gtc agc	748
Leu Ser Phe Pro Asp Val Leu Cys Leu Gly Leu Met Phe Trp Val Ser	
185 190 195	
agc tcc atg gtt tgc ata ctg cac agg cac aag cag cgg gtc cag cac	796
Ser Ser Met Val Cys Ile Leu His Arg His Lys Gln Arg Val Gln His	
200 205 210 215	
att gat agg agc gat ctc tcc ccc aga gcc tcc cca gag aac aga gct	844
Ile Asp Arg Ser Asp Leu Ser Pro Arg Ala Ser Pro Glu Asn Arg Ala	
220 225 230	
acg cag agc atc ctc atc ctg gtg agc acc ttt gtg tct tct tac act	892
Thr Gln Ser Ile Leu Ile Leu Val Ser Thr Phe Val Ser Ser Tyr Thr	
235 240 245	
ctc tcc tgc ctt ttc caa gtt tgt atg gct ctt ttg gat aat ccc aat	940
Leu Ser Cys Leu Phe Gln Val Cys Met Ala Leu Leu Asp Asn Pro Asn	
250 255 260	
agt tta ctg gtg aac act tca gcc tta atg agt gta tgt ttc cca act	988
Ser Leu Leu Val Asn Thr Ser Ala Leu Met Ser Val Cys Phe Pro Thr	
265 270 275	
ctc agc ccc ttt gtt ctc atg agc tgt gac ccc agt gta tac agg ttt	1036
Leu Ser Pro Phe Val Leu Met Ser Cys Asp Pro Ser Val Tyr Arg Phe	
280 285 290 295	
tgt ttt gcc tgg aaa aga tga caagatctcc taacctcatc ataaacatgt	1087
Cys Phe Ala Trp Lys Arg *	
300	
acattgtata tatttgcctca tggttcaatt gatgacttac tcttctgtgc cgcaacctgc	1147
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<212> PRT	
<213> Homo sapiens	
<400> 11	
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Val Gly Val Leu Gly Ser Phe Ser Val Leu Leu His Tyr Leu Ser Phe	
20 25 30	
Tyr Cys Thr Gly Cys Arg Leu Arg Ser Thr Asp Leu Ile Val Lys His	

35	40	45
Leu Ile Val Ala Asn Phe	Leu Ala Leu Arg Cys	Lys Gly Val Pro Gln
50	55	60
Thr Met Ala Ala Phe	Gly Val Arg Tyr Phe	Leu Asn Ala Leu Gly Cys
65	70	75
Lys Leu Val Phe Tyr	Leu His Arg Val Gly	Arg Gly Val Ser Ile Gly
85	90	95
Thr Thr Cys Leu Leu	Ser Val Phe Gln Val	Ile Thr Val Ser Ser Arg
100	105	110
Lys Ser Arg Trp Ala	Lys Leu Lys Glu Lys	Ala Pro Lys His Val Gly
115	120	125
Phe Ser Val Leu Leu	Cys Trp Ile Val Cys	Met Leu Val Asn Ile Ile
130	135	140
Phe Pro Met Tyr Val	Ala Gly Lys Trp Asn	Tyr Thr Asn Ile Thr Val
145	150	155
Asn Glu Asp Leu Gly	Tyr Cys Ser Gly Gly	Gly Asn Asn Lys Ile Ala
165	170	175
Gln Thr Leu Arg Ala	Met Leu Leu Ser Phe	Pro Asp Val Leu Cys Leu
180	185	190
Gly Leu Met Phe Trp	Val Ser Ser Ser Met	Val Cys Ile Leu His Arg
195	200	205
His Lys Gln Arg Val	Gln His Ile Asp Arg	Ser Asp Leu Ser Pro Arg
210	215	220
Ala Ser Pro Glu Asn	Arg Ala Thr Gln Ser	Ile Leu Ile Leu Val Ser
225	230	235
Thr Phe Val Ser Ser	Tyr Thr Leu Ser Cys	Leu Phe Gln Val Cys Met
245	250	255
Ala Leu Leu Asp Asn	Pro Asn Ser Leu Leu	Val Asn Thr Ser Ala Leu
260	265	270
Met Ser Val Cys Phe	Pro Thr Leu Ser Pro	Phe Val Leu Met Ser Cys
275	280	285
Asp Pro Ser Val Tyr	Arg Phe Cys Phe Ala	Trp Lys Arg
290	295	300

<210> 12
 <211> 906
 <212> DNA
 <213> Homo sapiens

<400> 12					
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120					
tccacagatt	tgattgttaa	gcacctgatt	gtagccaact	tcttagctct	ccgctgtaaa
180					
ggagtccccc	agacaatggc	agcttttggg	gtagatatt	ttctcaatgc	tcttgggtgc
240					
aaacttgttt	tctatctcca	tagagtgggc	aggggagtgt	ccattggcac	cacctgcctc
300					
ttgagtgtct	tccaggtgat	cacggtcagc	tccaggaaat	ccaggtgggc	aaaacttaaa
360					
gagaaagccc	ccaagcatgt	tggcttttct	gttctcctgt	gctggatcgt	gtgcatgttg
420					
gtaaacaatca	tctttcccat	gtatgtggct	ggcaaataga	actacacaaa	catcacagtg
480					
aacgaggatt	tggtgatactg	ttctggggga	ggcaacaaca	aaatcgca	gacactgcgt
540					
gcaatgttgt	tatcattccc	tgatgtgttg	tgtctggggc	tcatgttctg	ggtcagcagc
600					
tccatggttt	gcatactgca	caggcacaag	cagcgggtcc	agcacattga	taggagcgat
660					
ctctccccc	gagcctcccc	agagaacaga	gctacgcaga	gcacctcat	cctgggtgagc
720					
accttttgt	cttcttacac	tctctcctgc	cttttccaag	tttgtatggc	tcttttggtg
780					
aatcccaata	gtttactggg	gaacacttca	gccttaata	gtgtatgttt	cccaactctc
840					
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900					
agatga					906

<210> 13
 <211> 3492
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (73)...(2064)

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 Met Ser Trp Leu Ser Ser Ser Gln Gly Val Val Leu Thr
 1 5 10

gcc tac cac ccc agc ggc aag gac cag gcc gtc ggg aac agc cat gca 159
 Ala Tyr His Pro Ser Gly Lys Asp Gln Ala Val Gly Asn Ser His Ala
 15 20 25

aag gca ggg gag gaa gcc acc tcg agt cgc aga tat ggc cag tac act 207
 Lys Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr
 30 35 40 45

atg aac cag gaa agc acc acc atc aaa gtt atg gag aag cct cca ttt 255
 Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe
 50 55 60

gat cga tca att tcc cag gat tct ttg gat gaa cta tct atg gaa gac 303
 Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp
 65 70 75

tat tgg ata gaa cta gaa aac atc aag aaa tct agt gaa aac agc caa 351
 Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln
 80 85 90

gaa gat caa gag gtg gtt gtt gtc aaa gag cct gat gag gga gaa ttg 399
 Glu Asp Gln Glu Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu
 95 100 105

gaa gaa gag tgg ctt aaa gag gcc ggt tta tcc aat ctc ttc gga gag 447
 Glu Glu Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu
 110 115 120 125

tct gct gga gat cca cag gaa agc att gtg ttt tta tca aca ttg acg 495
 Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr
 130 135 140

cgg acc cag gca gca gca gtt cag aag cga gta gag acg gtc tcc cag 543
 Arg Thr Gln Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln
 145 150 155

acc ttg aga aaa aaa aac aaa cag tac cag att cct gac gtc aga gac 591
 Thr Leu Arg Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp
 160 165 170

ata ttt gct caa cag aga gaa tca aaa gaa aca gct cca ggt ggc act 639
 Ile Phe Ala Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr

175	180	185	
gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa gga aga gat			687
Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp			
190	195	200	205
gac gag gca tct aac ctt gtt ggt gaa gag aag ctg atc cca cct gag			735
Asp Glu Ala Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu			
	210	215	220
gag acg cct gcc cct gaa aca gac atc aac ctg gag gta tca ttt gcc			783
Glu Thr Pro Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala			
	225	230	235
gag caa gca ctc aat cag aaa gag agc tcc aag gag aaa atc cag aag			831
Glu Gln Ala Leu Asn Gln Lys Glu Ser Ser Lys Glu Lys Ile Gln Lys			
	240	245	250
agc aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca aaa gac			879
Ser Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp			
	255	260	265
aaa acg ggt acc aca agg att ggt gac ctc gca ccc cag gac atg aag			927
Lys Thr Gly Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys			
	270	275	280
aaa gtt tgc cat tta gcc cta att gag ctg act gcc ctc tat gat gta			975
Lys Val Cys His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val			
	290	295	300
ttg ggt att gag ctg aaa caa caa aaa gct gtg aaa atc aaa aca aaa			1023
Leu Gly Ile Glu Leu Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys			
	305	310	315
gat tct ggt ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa gat			1071
Asp Ser Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Glu Gln Asp			
	320	325	330
cag agg aaa gta cca gga atg cga ata ccc ttg atc ttt caa aaa ctg			1119
Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu			
	335	340	345
att tct cga att gaa gag aga ggt ttg gaa aca gaa ggc ctc tta cgg			1167
Ile Ser Arg Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg			
	350	355	360
atc cct gga gct gcc att aga atc aag aat ctt tgc caa gaa cta gaa			1215
Ile Pro Gly Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu			
	370	375	380
gca aag ttt tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat			1263
Ala Lys Phe Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His			
	385	390	395
gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg ccc cag cca			1311
Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro			
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ctg ctc agt gtg gag tat ctc aaa gcc ttt cag gct gtc cag aat ctt Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu 415 420 425	1359
cca acc aag aag cag caa cta cag gct ttg aac ctt ctt gtc atc ctc Pro Thr Lys Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Val Ile Leu 430 435 440 445	1407
cta cct gat gca aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc Leu Pro Asp Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu 450 455 460	1455
caa aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc atg aat Gln Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn 465 470 475	1503
gta gca atg gtc atg gcc ccg aat ctc ttt atg tgt cat gca ttg gga Val Ala Met Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly 480 485 490	1551
ttg aag tcc agt gaa cag cga gaa ttt gta atg gca gct ggg aca gca Leu Lys Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala 495 500 505	1599
aat acc atg cac tta ttg att aag tac caa aaa ctt ctg tgg aca att Asn Thr Met His Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile 510 515 520 525	1647
ccc aag ttt att gta aac caa gtg agg aag caa aac acg gaa aat cat Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His 530 535 540	1695
aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag aaa atg gct tat Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr 545 550 555	1743
gac cga gaa aaa tat gaa aag caa gat aag agt aca aat gat gct gac Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp 560 565 570	1791
gtt cct cag gga gtg att cga gtg caa gct ccc cat ctt tcg aaa gtt Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val 575 580 585	1839
tcc atg gca ata cag cta act gaa gaa cta aaa gcc agt gat gta ctt Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu 590 595 600 605	1887
gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act ctc aag aaa Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys 610 615 620	1935
gga gaa gtt ttt ttg tat gaa att gga gga aat att ggg gaa cgc tgc Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys 625 630 635	1983

ctt gat gat gac act tac atg aag gat tta tat cag ctt aac cca aat 2031
 Leu Asp Asp Asp Thr Tyr Met Lys Asp Leu Tyr Gln Leu Asn Pro Asn
 640 645 650

gct gag tgg gtt ata aag tca aag cca ttg tag aagacttaac aagctgcaga 2084
 Ala Glu Trp Val Ile Lys Ser Lys Pro Leu *
 655 660

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caggactcat	attattcagt	tgtacccaag	tatttataaa	tgactctctt	aagccttaaa	2204
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<210> 14
 <211> 663
 <212> PRT
 <213> Homo sapiens

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 Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln
 35 40 45
 Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser
 50 55 60
 Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile
 65 70 75 80
 Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln
 85 90 95
 Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu
 100 105 110
 Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly
 115 120 125
 Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr Arg Thr Gln
 130 135 140

Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln Thr Leu Arg
 145 150 155 160
 Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala
 165 170 175
 Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln
 180 185 190
 Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala
 195 200 205
 Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro
 210 215 220
 Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala
 225 230 235 240
 Leu Asn Gln Lys Glu Ser Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly
 245 250 255
 Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly
 260 265 270
 Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys Lys Val Cys
 275 280 285
 His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile
 290 295 300
 Glu Leu Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser Gly
 305 310 315 320
 Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys
 325 330 335
 Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg
 340 345 350
 Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly
 355 360 365
 Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
 370 375 380
 Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His Asp Ala Ala
 385 390 395 400
 Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser
 405 410 415
 Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys
 420 425 430
 Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp
 435 440 445
 Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val
 450 455 460
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 465 470 475 480
 Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys Ser
 485 490 495
 Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met
 500 505 510
 His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe
 515 520 525
 Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp
 530 535 540
 Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu
 545 550 555 560
 Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp Val Pro Gln
 565 570 575
 Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
 580 585 590
 Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe

	595		600		605	
Leu	Ser	Gln	Glu	Ser	Gly	Val
	610		615		620	
Phe	Leu	Tyr	Glu	Ile	Gly	Gly
625			630		635	
Asp	Thr	Tyr	Met	Lys	Asp	Leu
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Val	Ile	Lys	Ser	Lys	Pro	Leu
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<210> 15
 <211> 1992
 <212> DNA
 <213> Homo sapiens

<400> 15									
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gccagtgatg	tacttgccag	gtttctcagc	caagaaagtg	gggttgccca	gactctcaag				1860
aaaggagaag	tttttttgta	tgaaattgga	ggaaatattg	gggaacgctg	ccttgatgat				1920
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<210> 16
 <211> 502
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 16

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Leu	Leu	Ile	Thr	Val	Pro	Pro	Leu	Leu	Leu	Ala	Ile	Ala	Ala	Trp	Ile	20	25	30	
Gly	Leu	Glu	Glu	Ile	Lys	Glu	Trp	Lys	Lys	Ser	Pro	Leu	Tyr	Leu	Ser	35	40	45	
Asn	Asp	His	Glu	Leu	Asp	Val	Pro	Ile	Leu	Leu	Ile	Leu	Ser	Gln	Ala	50	55	60	
Pro	Gln	Gly	Ser	Arg	Phe	Pro	Thr	Leu	Glu	Glu	Asn	Arg	Ile	Leu	Leu	65	70	75	80
Trp	Thr	Trp	Pro	Phe	Asn	Asp	Arg	Gly	Ala	Pro	Val	Pro	Pro	Ser	Arg	85	90	95	
Cys	Ser	Leu	Ser	Tyr	Asp	Asn	Thr	Ala	Arg	Cys	Arg	Leu	Thr	Ala	Asn	100	105	110	
Arg	Ser	Glu	Leu	Glu	Ser	Ala	Asp	Ala	Val	Leu	Phe	Asn	Ala	Gly	His	115	120	125	
His	Arg	Asp	Leu	Ser	Lys	Gly	Pro	Pro	Met	Asp	Leu	Pro	Pro	Glu	Phe	130	135	140	
Thr	Gln	Val	Arg	Ala	Arg	Ala	Glu	Asp	Ala	Asp	Ala	Val	Leu	Leu	Ala	145	150	155	160
Tyr	Glu	Asp	Asn	Ala	Ala	Ala	Ala	Glu	Ala	Leu	Ala	Thr	Asp	Phe	Pro	165	170	175	
Arg	Pro	Pro	Gly	Gln	Pro	Trp	Val	Trp	Ala	Ser	Met	Glu	Ser	Pro	Ser	180	185	190	
Asn	Ser	Gly	Arg	Phe	Ala	Val	Pro	Gly	Phe	Lys	Ile	Asn	Val	Leu	Asn	195	200	205	
Gly	Leu	Gln	Ile	Leu	Leu	Asp	Gly	Tyr	Phe	Asn	Trp	Thr	Leu	Ser	Tyr	210	215	220	
Arg	Ala	Asp	Ser	Asp	Ala	Phe	His	Pro	Tyr	Gly	Tyr	Leu	Glu	Pro	Leu	225	230	235	240
Thr	Ala	Lys	Ala	Arg	Lys	Arg	Gly	Phe	Lys	Val	Gln	Ser	Gln	Val	Val	245	250	255	
Glu	Ala	Pro	Leu	Asn	Leu	Ser	Ala	Lys	Ala	Lys	Leu	Ala	Ala	Trp	Val	260	265	270	
Val	Ser	Asn	Cys	Asn	Thr	Arg	Ser	Lys	Arg	Glu	Arg	Phe	Tyr	Lys	Gln	275	280	285	
Leu	Lys	Lys	His	Leu	Gln	Val	Asp	Val	Tyr	Gly	Arg	Val	Ala	Asn	Pro	290	295	300	
Leu	Pro	Leu	Lys	Ser	Gly	Cys	Ser	Lys	Gly	Val	Glu	Leu	Ile	Glu	Thr	305	310	315	320
Leu	Ser	Gln	Tyr	Lys	Phe	Tyr	Leu	Ala	Phe	Glu	Asn	Ser	Gln	His	Glu	325	330	335	
Asp	Tyr	Val	Thr	Glu	Lys	Leu	Trp	Lys	Asn	Ala	Leu	Gln	Ala	Gly	Thr	340	345	350	
Ile	Pro	Val	Val	Leu	Gly	Pro	Ser	Arg	Ala	Val	Tyr	Glu	Asp	Phe	Val	355	360	365	
Pro	Pro	Lys	Ser	Phe	Ile	His	Val	Asp	Asp	Phe	Lys	Ser	Ala	Lys	Glu	370	375	380	
Leu	Ala	Asp	Tyr	Leu	Leu	Tyr	Leu	Asp	Lys	Asn	Pro	Thr	Ala	Tyr	Leu	385	390	395	400
Asp	Met	Leu	Tyr	Glu	Asn	Pro	Leu	Asn	Thr	Leu	Asp	Gly	Lys	Ala	Tyr	405	410	415	
Phe	Tyr	Gln	Asp	Leu	Ser	Phe	Lys	Lys	Ile	Leu	Asp	Phe	Phe	Lys	Thr	420	425	430	

Ile Leu Glu Asn Asp Thr Ile Tyr His Lys Tyr Ser Glu Tyr Phe Glu
435 440 445
Trp Arg Glu Asp Leu Arg Val Arg Leu Phe Ser Trp Asp Ala Leu Arg
450 455 460
Val Leu Glu Tyr Asp Glu Gly Phe Cys Arg Val Cys Arg Leu Leu Gln
465 470 475 480
Lys Ala Pro Asp Leu Leu Glu Leu Ser Arg Tyr Lys Thr Ile Pro Asn
485 490 495
Leu Ala Lys Trp Phe Gln
500

<210> 17
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

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20 25 30
Ser Arg Arg Pro Trp Ala Arg Gly Val Leu Phe Tyr Gly Ser Asn Ile
35 40 45
Lys Thr Gly Asp Phe Pro Leu Pro Arg Asn Glu His Gln Ile Trp Ala
50 55 60
Leu Leu His Glu Glu Ser Pro Arg Asn Thr Pro Phe Val Ser Asn Lys
65 70 75 80
Glu Phe Leu Arg His Phe His Phe Thr Ser Thr Phe Ser Arg Tyr Ser
85 90 95
Asn Leu Pro Leu Thr Thr Met Tyr Leu Pro Ser Gly Glu Ala Leu Thr
100 105 110
Ser Lys Asp Tyr Tyr Val Thr Phe Asp Gly Lys Ser Lys Tyr Gly Tyr
115 120 125
Arg Pro Ser Thr Ser Val Val Phe Leu Gln Ser Asp Cys Asp Thr Met
130 135 140
Ser Gly Arg Glu Asp Tyr Val Lys Glu Leu Met Lys His Leu Pro Ile
145 150 155 160
Asp Ser Tyr Gly Ser Cys Leu Arg Asn Arg Asp Leu Pro Glu Arg Gln
165 170 175
Lys Asp

<210> 18
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
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Val Ala Trp Val Val Ser Asn Trp Asn Pro Asn Ser Ala Arg Val Arg
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Tyr Tyr Gln Gln Leu Gln Lys His Leu Lys Val Asp Val Tyr Gly Arg

Arg Arg Tyr Phe Trp Trp His Ser Ile Tyr Arg Leu Arg Lys Thr Ser
260 265 270
Gln Pro Tyr Cys Ala Leu Cys Ser Leu Ile Gln Gln Ser Pro Gly Gly
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His Glu Val Arg Gln Arg Ser Tyr
290 295

<210> 20
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 20
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Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
20 25 30
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
35 40 45
Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
50 55 60
Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
65 70 75 80
Ser

<210> 21
<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 21
Lys Val Val Ile Leu Leu Val Trp Val Leu Ala Leu Leu Leu Ser Leu
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Pro Pro Leu Leu Phe Ser Trp Val Lys Thr Val Glu Glu Gly Asn Gly
20 25 30
Thr Leu Asn Val Asn Val Thr Val Cys Leu Ile Asp Phe Pro Glu Glu
35 40 45
Ser Thr Ala Ser Val Ser Thr Trp Leu Arg Ser Tyr Val Leu Leu Ser
50 55 60
Thr Leu Val Gly Phe Leu Leu Pro Leu Leu Val Ile Leu Val Cys Tyr
65 70 75 80
Thr Arg Ile Leu Arg Thr Leu Arg Lys Ala Ala Lys Thr Leu Leu Val
85 90 95
Val Val Val Val Phe Val Leu Cys Trp Leu Pro Tyr Phe Ile Val Leu
100 105 110
Leu Leu Asp Thr Leu Cys Leu Ser Ile Ile Met Ser Ser Thr Cys Glu
115 120 125
Leu Glu Arg Val Leu Pro Thr Ala Leu Leu Val Thr Leu Trp Leu Ala
130 135 140
Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr

155

<220>
<223> Consensus amino acid sequence

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<211> 108
<212> PRT
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<220>
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<210> 24
<211> 183
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<220>
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<400> 24
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 Leu Leu Ala Gly Val Ile Lys Lys Tyr Arg Trp Gly Met Lys Met Ala
 35 40 45
 Leu Leu Phe His Leu Cys Val Thr Gly Ala Leu Leu Ser Ile Thr Asn
 50 55 60
 Thr Leu His Leu Leu Ala Ser Gly Tyr His Leu Leu Lys Arg Gln Arg
 65 70 75 80
 Asn Ser Ser Thr Val Leu Gln Ser Phe Ala Ile Ile Ala Trp Val Asp
 85 90 95
 His Phe Ile Gly Phe Ala Leu Leu Ile Phe Val Met Tyr Leu Ala Ile
 100 105 110
 Phe Cys Phe Lys Phe Tyr Trp Asn Asn Lys Thr Arg Ser Ile Glu Trp
 115 120 125
 Gly Arg Ser Tyr Val Leu Tyr Ala Ile Ser Thr Trp Val Ile Ala Phe
 130 135 140
 Leu Ile Ala Gly Phe Thr Ala Phe Phe Gln Cys Asp Ser His Ile Asn
 145 150 155 160
 Ser Gln Asp Gln Cys Ile Gln Ile Val Cys Ala Val Ser Asn Ile Phe
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 Ser Ala Ile Phe Thr Glu Leu
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<210> 25

<211> 259

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 25

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
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 20 25 30
 Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
 35 40 45
 Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
 50 55 60
 Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
 65 70 75 80
 Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
 85 90 95
 Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
 100 105 110
 Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
 115 120 125
 Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
 130 135 140
 Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
 145 150 155 160
 Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
 165 170 175
 Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
 180 185 190
 Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe Val Leu Cys

195 200 205
 Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
 210 215 220
 Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
 225 230 235 240
 Leu Leu Val Thr Leu Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro
 245 250 255
 Ile Ile Tyr

<210> 26
 <211> 182
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 26
 Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu Ser Trp Leu Gly Phe
 1 5 10 15
 His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser Arg Arg Pro Asp Glu
 20 25 30
 Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe His Ala Leu Ser Phe
 35 40 45
 Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr Leu Lys Val Leu Lys
 50 55 60
 Val Ala Arg Phe His Cys Lys Arg Ile Asp Val Ile Thr Met Gln Thr
 65 70 75 80
 Leu Val Leu Leu Val Asp Ile His Pro Ser Val Arg Glu Arg Cys Leu
 85 90 95
 Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr Lys Lys Ile Ser Thr
 100 105 110
 Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro Tyr Val Ile Thr Arg
 115 120 125
 Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Asp Ser His Trp Gly Val
 130 135 140
 Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala Ser Asp Pro Phe Val
 145 150 155 160
 Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser Cys Lys Glu Leu Leu
 165 170 175
 Asn Arg Ile Phe Asn Arg
 180

<210> 27
 <211> 157
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 27
 Thr Leu Phe Ile Val Gly Phe Met Ile Pro Cys Leu Val Ile Ile Val
 1 5 10 15
 Cys Tyr Ala Cys Ile Phe Leu Thr Val His His Gln Lys Lys Lys Ile
 20 25 30

Arg Asn His Asp Asn Phe Gln Ile Ala Ala Ala Lys Gly Ser Ser Ser
 35 40 45
 Ser Gly Gly Gly Ser Tyr Met Thr Thr Thr Cys Thr Arg Lys Ala Arg
 50 55 60
 Glu Asp Arg Lys Thr Thr Lys Met Leu Met Val Val Phe Leu Cys Phe
 65 70 75 80
 Ala Ile Cys Tyr Leu Pro Ile Ser Ile Leu Asn Val Leu Lys Arg Val
 85 90 95
 Phe Gly Met Phe Arg His Ser Glu Asp Asn Glu Ser Val Tyr Trp Trp
 100 105 110
 His Ile Phe Ser His Trp Leu Val Tyr Ala Asn Ser Cys Ile Asn Pro
 115 120 125
 Ile Ile Tyr Asn Phe Met Asn Gly Lys Tyr Arg Lys Ala Tyr Trp Lys
 130 135 140
 Ile Phe Ala Leu Leu Lys Phe Trp Gly Glu Pro Leu Ser
 145 150 155

<210> 28
 <211> 160
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 28
 Ala Tyr Val Val Met Leu Val Val Ala Val Phe Phe Ile Pro Phe Ser
 1 5 10 15
 Val Met Leu Tyr Ser Tyr Met Cys Ile Leu Asn Thr Val Arg His Asn
 20 25 30
 Ala Val Arg Ile His Asn His Pro Asp Ser Leu Cys Leu Ser Gln Val
 35 40 45
 Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro His Gln Met Ser Val
 50 55 60
 Asp Met Ser Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe
 65 70 75 80
 Val Gly Phe Ser Leu Cys Trp Leu Pro His Ser Val Tyr Ser Leu Leu
 85 90 95
 Ser Val Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Tyr Glu Ile
 100 105 110
 Ser Thr Cys Val Leu Trp Leu Cys Tyr Leu Lys Ser Val Phe Asn Pro
 115 120 125
 Ile Ile Tyr Cys Trp Arg Ile Lys Lys Phe Arg Glu Ala Cys Leu Glu
 130 135 140
 Met Met Pro Lys Thr Phe Lys Ile Leu Pro Gln Val Pro Gly Arg Thr
 145 150 155 160

<210> 29
 <211> 93
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 29
 His Lys Ile Ile Lys Ala Ala Cys Leu Val Gln Gln Lys Arg Gln Glu

1		5		10		15									
Phe	Leu	Ala	Ser	Val	Ala	Arg	Gly	Val	Ala	Pro	Ala	Asp	Ser	Pro	Glu
	20				25				30						
Ala	Pro	Arg	Arg	Ser	Phe	Ala	Gly	Gly	Thr	Trp	Asp	Trp	Glu	Tyr	Leu
	35				40				45						
Gly	Phe	Ala	Ser	Pro	Glu	Glu	Tyr	Ala	Glu	Phe	Gln	Tyr	Arg	Arg	Arg
	50				55				60						
His	Arg	Gln	Arg	Arg	Arg	Gly	Asp	Val	His	Ser	Leu	Leu	Ser	Asn	Pro
65				70					75					80	
Pro	Asp	Pro	Asp	Glu	Pro	Ser	Glu	Ser	Thr	Leu	Asp	Ile			
			85				90								

<210> 30
 <211> 33
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400>	30														
Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Val	Cys	Tyr	Thr	Arg	Ile	Leu	Arg
1	5	10	15												
Thr	Leu	Arg	Lys	Ala	Ala	Lys	Thr	Leu	Val	Val	Val	Val	Val	Val	Phe
	20						25					30			
Val															

<210> 31
 <211> 260
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400>	31														
Gly	His	Arg	Ser	Arg	Pro	Thr	Asp	Leu	Pro	Ile	Gly	Leu	Leu	Ser	Leu
1	5	10	15												
Val	His	Leu	Met	Met	Leu	Leu	Thr	Met	Gly	Phe	Ile	Ala	Thr	Met	Asp
	20						25					30			
Met	Phe	Met	Ser	Trp	Gly	Arg	Trp	Asp	Asp	Thr	Thr	Cys	Lys	Ser	Leu
	35						40					45			
Ile	Tyr	Leu	His	Arg	Leu	Leu	Arg	Gly	Leu	Ser	Leu	Cys	Thr	Thr	Cys
	50				55				60						
Leu	Leu	Asn	Val	Phe	Gln	Ala	Ile	Thr	Leu	Ser	Pro	Arg	Ser	Ser	Cys
65			70						75					80	
Leu	Ala	Lys	Phe	Lys	His	Lys	Ser	Pro	His	His	Ile	Ser	Cys	Ala	Phe
			85					90					95		
Leu	Phe	Leu	Trp	Val	Leu	Tyr	Met	Ser	Phe	Ser	Ser	His	Leu	Leu	Leu
	100						105					110			
Ser	Ile	Ile	Ala	Thr	Pro	Asn	Leu	Thr	Ser	Asn	Asp	Phe	Met	Tyr	Val
	115						120					125			
Thr	Gln	Ser	Cys	Ser	Ile	Leu	Pro	Met	Ser	Tyr	Ser	Met	Gln	Ser	Met
	130					135					140				
Phe	Ser	Thr	Leu	Leu	Ala	Ile	Arg	Asp	Val	Phe	Leu	Ile	Gly	Leu	Met
145				150					155					160	

Val Leu Ser Ser Gly Tyr Met Val Ala Leu Leu Cys Arg His Arg Lys
 165 170 175
 Gln Ala Gln His Leu His Ser Thr Ser Leu Ser Pro Lys Ala Ser Pro
 180 185 190
 Glu Gln Arg Ala Thr Arg Thr Ile Leu Met Leu Met Ser Ser Phe Phe
 195 200 205
 Val Leu Met Tyr Ile Phe Asp Ser Ile Val Phe Cys Ser Arg Thr Met
 210 215 220
 Phe Lys Asp Gly Pro Thr Phe Tyr Cys Ile Gln Ile Ile Val Ser His
 225 230 235 240
 Ser Tyr Ala Thr Val Ser Pro Phe Val Phe Ile Cys Thr Glu Lys His
 245 250 255
 Ile Val Lys Phe
 260

<210> 32
 <211> 170
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid

<400> 32
 Pro Ile Ile Val Glu Lys Cys Val Glu Tyr Ile Glu Lys Leu Tyr Pro
 1 5 10 15
 Leu Ala Glu Arg Gly Leu Gln Glu Glu Gly Ile Tyr Arg Val Ser Gly
 20 25 30
 Ser Ala Ser Arg Val Lys Glu Leu Arg Glu Ala Phe Asp Lys Asp Gly
 35 40 45
 Ala Pro Asp Ser Leu Glu Leu Ser Glu Lys Glu Trp Phe Asp Val His
 50 55 60
 Val Val Ala Gly Leu Leu Lys Leu Tyr Leu Arg Glu Leu Pro Glu Pro
 65 70 75 80
 Leu Ile Pro Tyr Asp Leu Tyr Glu Glu Phe Ile Arg Ala Ala Lys Glu
 85 90 95
 Gln Ile Glu Asp Pro Asp Glu Arg Leu Arg Ala Leu Lys Glu Leu Leu
 100 105 110
 Ser Ser Lys Leu Pro Arg Ala His Tyr Asn Thr Leu Arg Tyr Leu Leu
 115 120 125
 Thr His Leu Asn Arg Val Ala Glu Ile Tyr Ile Glu Asn Ser Ala Val
 130 135 140
 Asn Lys Met Asn Ala Arg Asn Leu Ala Ile Val Phe Gly Pro Thr Leu
 145 150 155 160
 Leu Arg Pro Pro Asp Lys Glu Ser Asn Asp
 165 170

<210> 33
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 33
 Leu Lys Tyr Gln Lys Ile Leu Trp Lys Val Pro Ser Phe Leu Ile Thr

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      1           5           10           15
Gln Val Arg Arg Met Asn Glu Ala Thr Met Leu Leu Lys Lys Gln Leu
      20           25           30
Pro Ser Val Arg Lys Leu Leu Arg Arg Lys Thr Leu Glu Arg Glu Thr
      35           40           45
Ala Ser Pro Lys Thr Ser Lys Val Leu Gln Lys Ser Pro Ser Ala Arg
      50           55           60
Arg Met Ser Asp Val Pro Glu Gly Val Ile Arg Val His Ala Pro Leu
      65           70           75           80
Leu Ser Lys Val Ser Met Ala Ile Gln Leu Asn Asn Gln Thr Lys Ala
      85           90           95
Lys Asp Ile Leu Ala Lys Phe
      100

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<210> 34
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

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<400> 34
Asn Met Glu Glu Tyr Glu Asp Val His Thr Val Ala Gly Leu Leu Lys
      1           5           10           15
Gln Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Tyr Glu Leu Tyr
      20           25           30
Glu Glu Phe Ile Glu Ala Ala Lys Ala Gln Val Ser Asp Glu Asp Glu
      35           40           45
Arg Met Glu Ala Leu Glu Met Leu Lys Glu Leu Ile Lys Leu Leu Pro
      50           55           60
Glu Ala Asn Arg Glu Thr Leu Arg Tyr Leu Leu Lys His Leu Ser Arg
      65           70           75           80
Val Ala Gln His Ser Glu Glu Asn Lys Met Asn Ala Gln Asn Leu Ala
      85           90           95
Val Val Phe Gly Pro Thr Leu
      100

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<210> 35
 <211> 90
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

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<400> 35
Ala Cys Ser Leu Leu Lys Leu Phe Leu Arg Glu Leu Pro Glu Pro Leu
      1           5           10           15
Leu Thr Thr Asp Leu Val Ala Arg Phe Glu Glu Val Ala Ser His Pro
      20           25           30
Lys Val Thr Thr Gln Gln Ala Glu Leu Gln Gln Leu Leu Glu Gln Leu
      35           40           45
Pro Lys Cys Asn Arg Thr Leu Leu Ala Trp Val Leu Leu His Phe Asp
      50           55           60
Ala Val Ile Gln Gln Glu Arg His Asn Lys Leu Asn Ala Gln Ser Leu
      65           70           75           80

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Ala Met Leu Leu Ser Pro Thr Leu Gln Met
85 90

<210> 36
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<221> VARIANT
<222> (1)...(79)
<223> Xaa = Any Amino Acid

<400> 36
Gly Ser Thr Ala Leu Ile Val Met Phe Tyr Trp Cys Gly Ser Thr Ala
1 5 10 15
Asn Cys Pro Asp Glu Glu Asp Pro Lys Arg His Xaa Xaa Leu Ile Val
20 25 30
Met Asn Gln Gly Ala Xaa Xaa Leu Ile Val Met Phe Thr Gly Ser Thr
35 40 45
Ala Asn Cys Leu Ile Val Met Phe Tyr Trp Ser Thr Ala Cys Asp Glu
50 55 60
Asn His Arg Phe Tyr Trp Cys Ser His Xaa Xaa Leu Ile Val Met
65 70 75

<210> 37
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<221> VARIANT
<222> (1)...(50)
<223> Xaa = Any Amino Acid

<400> 37
Leu Ile Val Met Phe Trp Ala Cys Pro Gly Ala Cys Xaa Xaa Xaa Ser
1 5 10 15
Ala Cys Lys Ser Thr Ala Leu Ile Met Arg Gly Ser Ala Cys Pro Asn
20 25 30
Val Ser Thr Ala Cys Pro Xaa Xaa Asp Glu Asn Phe Ala Pro Xaa Xaa
35 40 45
Ile Tyr
50